Geuvadis RNA-seq conference call minutes

November 3, 2011

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RNA Samples

* Total 465 samples with RNA
* **Samples will be shipped to the partners on the week starting on November 7 or November 14.** Tuuli has all the contact information of the people responsible for receiving the samples
* The samples will be shipped to the partners with codes, not the real IDs

Sequencing guidelines

* Tuuli presented the draft summarizing the guidelines for sequencing (seq\_protocol\_summary\_draft.docx). The final version will be sent to the partners by November 10.
* As most decisions were according to the suggestions in that text, they’re not rewritten here. The issues that raised some discussion:
  + The fragment size of mRNA needs to be specified. Tuuli will inform everyone about this later
  + The initial agreement for mRNAseq was to aim for coverage of 15-20M mapped reads. It was now specified that this means a minimum of **10M mapped and properly paired read pairs.**
  + How to define what counts as a mapped read pair in mRNAseq: all the labs should **map the data for quality control purposes by mapping the first 50 bp of the reads to the genome using bwa or an equivalent mapper.** 50 bp was chosen because there is more evidence of that than mapping 75bp reads. Samples that have less than 10M properly paired read pairs should be rerun.
  + Barcelona will provide Tuuli with more detailed specification of the miRNAseq protocol within a few days
  + The deadline for submission of the fastq files to EBI is February 15, 2011

Iberian cell lines

* The initial plan in the project was to analyze 100 IBS samples, but they were not available from Coriell before – but now they are. If many partners would have wanted to have these cell lines, they could be added to the cell banks (but not this RNAseq experiment) of the project. No one expressed great interest these samples, so we **decided not to add the Iberian samples to our cell banks.**

Analysis group

* We need to **put together an analysis group** as soon as possible so that we can start planning data analysis well before we have the data in our hands. Everyone is invited to contribute to this
* Garbielle will help to set up a mailing list – there might be one from the pilot already

RNAseq wiki

* Tuuli has **set up a wiki for WP4** on the Geuvadis intranet. It will contain the documents and information that are (and have been) distributed by email about protocols, samples, structure of the project, etc. Once we get to the analysis phase it will be the place to share methods and results

1000 genomes collaboration

* Tuuli gave a brief account of the discussions she had about Geuvadis at the 1000 Genomes project meeting in Montreal. Many people showed interest in the work that we are doing. 1000g Phase 1 paper will not include much functional analysis, but it remains to be seen what will happen later, and whether we might want to collaborate with some people from the functional interpretation group.

Next TC

* We will meet in Toulouse, and will see later if there is a need for another call around that time

**Action items**

* **Tuuli** will take care of the RNA sample shipments (7/14 November) and inform the contact persons from each lab when the samples are shipped
* **Esther** from Barcelona will email Tuuli further specifications of the miRNAseq protocol, including the minimum coverage per sample and how exactly that is defined
* **Tuuli** will send the final version of the sequencing guidelines to all the labs by November 10
* **Gabrielle** will set up a mailing list for the analysis group
* After the labs have received the samples, there is one major action item for **all partners**: sequencing!